

Query= SEQ ID NO:6
 (1110 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AC113382.2.1.166870	<u>1084</u>	0.0
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>AC113382.2.1.166870
 Length = 166870

Score = 1084 bits (547), Expect = 0.0
 Identities = 547/547 (100%)
 Strand = Plus / Minus

Query: 564	ggcagtgagagccaccatgaaaaggacatgcaaattgcatggcatctctgggagctgcag	623
Sbjct: 80777	ggcagtgagagccaccatgaaaaggacatgcaaattgcatggcatctctgggagctgcag	80718

Query: 624	catacagacatgctggctgcagctggctgaattccgggagatgggagactacctaaaggc	683
Sbjct: 80717	catacagacatgctggctgcagctggctgaattccgggagatgggagactacctaaaggc	80658

Query: 684	caagtatgaccaggcgctgaaaattgaaatggataagcggcagctgagagctgggaacag	743
Sbjct: 80657	caagtatgaccaggcgctgaaaattgaaatggataagcggcagctgagagctgggaacag	80598

Query: 744	cgccgagggccactgggtgcccgcctgaggccttccttcctagcgcagaggcggaactgat	803
Sbjct: 80597	cgccgagggccactgggtgcccgcctgaggccttccttcctagcgcagaggcggaactgat	80538

Query: 804	cttttttagaggaatcaccagattactgtacctgcaattccagcctgggcatctatggcac	863
Sbjct: 80537	cttttttagaggaatcaccagattactgtacctgcaattccagcctgggcatctatggcac	80478

Query: 864	agagggctcgtgagtgacctacagaacagccacaacacatccaggtgggagcgacgtagctg	923
Sbjct: 80477	agagggctcgtgagtgacctacagaacagccacaacacatccaggtgggagcgacgtagctg	80418

Query: 924	tgggcgcctgtgcactgagtggtggctgcaggtggaagagaggaaaactgaggtcataag	983
Sbjct: 80417	tgggcgcctgtgcactgagtggtggctgcaggtggaagagaggaaaactgaggtcataag	80358

Query: 984	cagctgtaactgcaaattccagtggtgctgtacgggtcaagtgtgaccagtgtaggcattgt	1043
Sbjct: 80357	cagctgtaactgcaaattccagtggtgctgtacgggtcaagtgtgaccagtgtaggcattgt	80298

Query: 1044 ggtgagcaagtattactgcgacgctccccaggcagtgcccagtcctgggtaagggcag 1103
|||||
Sbjct: 80297 ggtgagcaagtattactgcgacgctccccaggcagtgcccagtcctgggtaagggcag 80238

Query: 1104 tgcctga 1110
|||||
Sbjct: 80237 tgcctga 80231

Score = 311 bits (157), Expect = 5e-82
Identities = 157/157 (100%)
Strand = Plus / Minus

Query: 1 atgctgtgctgcattcagtgccctctgacctggaagtcctttcccaaccctcactccttgc 60
|||||
Sbjct: 87176 atgctgtgctgcattcagtgccctctgacctggaagtcctttcccaaccctcactccttgc 87117

Query: 61 caaggaggccccattgtctcatccccattcacctctgacctactttttctctttttggt 120
|||||
Sbjct: 87116 caaggaggccccattgtctcatccccattcacctctgacctactttttctctttttggt 87057

Query: 121 aggtcagtgacaatttcctgataacagggtcccaagg 157
|||||
Sbjct: 87056 aggtcagtgacaatttcctgataacagggtcccaagg 87020

Score = 289 bits (146), Expect = 2e-75
Identities = 146/146 (100%)
Strand = Plus / Minus

Query: 420 aggaggccatggctggatctggggaggctgcagcgacaatgtggaatttggggaaaggat 479
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Sbjct: 82379 aggaggccatggctggatctggggaggctgcagcgacaatgtggaatttggggaaaggat 82320

Query: 480 ctccaaactctttgtggacagtttgaggagaaggggaaggatgccagagccctgatgaatct 539
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Query: 540 tcacaacaacagggccggcagactgg 565
|||||
Sbjct: 82259 tcacaacaacagggccggcagactgg 82234

Score = 280 bits (141), Expect = 2e-72
Identities = 141/141 (100%)
Strand = Plus / Minus

Query: 155 aggcctatctgacctacacgactagtgtggccttgggtgcccagagtggcatcgaggagt 214
|||||
Sbjct: 86808 aggcctatctgacctacacgactagtgtggccttgggtgcccagagtggcatcgaggagt 86749

Query: 215 gcaagttccagtttgcttgggaacgctggaactgccctgaaaatgctcttcagctctcca 274
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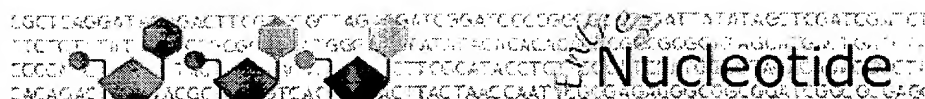
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Sbjct: 86688 cccacaacaggctgagaagtg 86668

Score = 254 bits (128), Expect = 1e-64
Identities = 128/128 (100%)
Strand = Plus / Minus

Query: 295 gctaccagagagacttccttcatacatgctatcagctctgctggagtcatgtacatcatc 354
|||||
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Query: 355 accaagaactgtagcatgggtgacttcgaaaactgtggctgtgatgggtcaaacaatgga 414
|||||
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Query: 415 aaaacagg 422
|||||
Sbjct: 83379 aaaacagg 83372



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Show:

☐ 1: [AC113382](#). Homo sapiens chro...[gi:27923635][Links](#)

LOCUS AC113382 166870 bp DNA linear PRI 28-JAN-2003

DEFINITION Homo sapiens chromosome 5 clone RP11-325L7, complete sequence.

ACCESSION AC113382

VERSION AC113382.2 GI:27923635

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 166870)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 166870)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 166870)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USACOMMENT On Jan 28, 2003 this sequence version replaced [gi:19033496](#).Draft Sequence Produced by DOE Joint Genome Institute
[www.jgi.doe.gov](#)

Finishing Completed at Stanford Human Genome Center

[www-shgc.stanford.edu](#)

Quality: Phrap Quality >=40 99.8% of Sequence;

Estimated Total Number of Errors is 0.2.

FEATURES

Location/Qualifiers

source

1..166870

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="RP11-325L7"

ORIGIN

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121 tttttttttt caattttcca cagacggaaa cgaggtgaaa agggagaagt ggtggaaact
181 gttgaagatg ttattgttcg gaaattgact gctgagcgag ttgaagaact aaagaaagtg
241 ataaaggaaa cccaggagag ataataggtac ttatcagaga gaatgcaaaa aaattgagaa
301 agacataagg gactgtcttc tggtagctgg cagaactttt aaaatagcag attaaaaaac
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